



AW

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,481  
Source: PCT09  
Date Processed by STIC: 7/24/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/647,481

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply PCT09  
Corrected Diskette Needed

## RAW SEQUENCE LISTING

DATE: 07/24/2002

PATENT APPLICATION: US/09/647,481

TIME: 11:25:53

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\07242002\I647481.raw

2 <110> APPLICANT: Ahmad, Sultan  
3 Hoffert, Cyrla  
4 O'Donnell, Dajan  
5 Pelletier, Manon  
6 Walker, Philippe  
8 <120> TITLE OF INVENTION: B1C3 G Protein-Coupled Receptor  
W--> 9 <130> FILE REFERENCE: walker 6  
W--> 10 <140> CURRENT APPLICATION NUMBER:  
C--> 11 <141> CURRENT FILING DATE: 2000-09-29  
W--> 12 <160> NUMBER OF SEQ ID: 6  
13 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

W--> 14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 400  
16 <212> TYPE: PRT  
17 <213> ORGANISM: Rat  
W--> 18 <400> SEQUENCE: 1  
19 Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val  
20 1 5 10 15  
21 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro  
E--> 22 20 25 30  
23 Gly Ala Gly Leu Arg Ala Asp Ala Ala Val Cys Leu Ala Val Cys Ala  
E--> 24 35 40 45  
25 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His  
E--> 26 50 55 60  
27 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu  
E--> 28 65 70 75 80  
29 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Thr Asn Ile Leu Leu Ser  
E--> 30 85 90 95  
31 Gly Pro Leu Thr Leu Arg Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu  
E--> 32 100 105 110  
33 Gly Gly Val Phe Val Ala Leu Ala Ala Ser Val Leu Ser Leu Leu Ala  
E--> 34 115 120 125  
35 Ile Ala Leu Glu Arg His Leu Thr Met Ala Arg Arg Gly Pro Ala Pro  
E--> 36 130 135 140  
37 Ala Ala Ser Arg Ala Arg Thr Leu Ala Met Ala Val Ala Ala Trp Gly  
E--> 38 145 150 155 160  
39 Leu Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu  
E--> 40 165 170 175  
41 Gly Arg Leu Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala

*amino numbering  
misaligned, see error  
summary sheet item 2*

## RAW SEQUENCE LISTING

DATE: 07/24/2002

PATENT APPLICATION: US/09/647,481

TIME: 11:25:53

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\07242002\I647481.raw

```

E--> 42 180                185                190
      43 Tyr Val Leu Phe Cys Val Leu Ala Phe Leu Gly Ile Leu Ala Ala Ile
E--> 44 195                200                205
      45 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
E--> 46 210                215                220
      47 Arg Leu Arg Ala Gly Pro Gly Ser Arg Arg Ala Thr Ser Ser Ser Arg
E--> 48 225                230                235                240
      49 Ser Arg His Thr Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val
E--> 50 245                250                255
      51 Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu
E--> 52 260                265                270
      53 Leu Leu Asp Val Ala Cys Pro Ala Arg Ala Cys Pro Val Leu Leu Gln
E--> 54 275                280                285
      55 Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro
E--> 56 290                295                300
      57 Ile Ile Tyr Thr Phe Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg
E--> 58 305                310                315                320
      59 Leu Leu Cys Cys Gly Arg Gly Pro Cys Asn Gln Asp Ser Ser Asn Ser
E--> 60 325                330                335
      61 Leu Gln Arg Ser Pro Ser Ala Val Gly Pro Ser Gly Gly Gly Leu Arg
E--> 62 340                345                350
      63 Arg Cys Leu Pro Pro Thr Leu Asp Arg Ser Ser Ser Pro Ser Glu His
E--> 64 355                360                365
      65 Ser Cys Pro Gln Arg Asp Gly Met Asp Thr Ser Cys Ser Thr Gly Ser
E--> 66 370                375                380
      67 Pro Gly Ala Ala Thr Ala Asn Arg Thr Leu Val Pro Asp Ala Thr Asp
E--> 68 385                390                395                400
      114 <210> SEQ ID NO: 6
      115 <211> LENGTH: 19
      116 <212> TYPE: DNA
      117 <213> ORGANISM: PCR primer
W--> 118 <400> SEQUENCE: 6
      119 caggagcagg ccaaacagg
W--> 122 ??
W--> 123 (... continued)
W--> 125 (... continued)
E--> 128 30044116v1

```

*mislabeled numbering*

19

*delete*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/647,481

DATE: 07/24/2002

TIME: 11:25:54

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\07242002\I647481.raw

L:9 M:283 W: Missing Blank Line separator, <130> field identifier  
L:10 M:283 W: Missing Blank Line separator, <140> field identifier  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:12 M:283 W: Missing Blank Line separator, <160> field identifier  
L:14 M:283 W: Missing Blank Line separator, <210> field identifier  
L:18 M:283 W: Missing Blank Line separator, <400> field identifier  
L:22 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
M:332 Repeated in SeqNo=1  
L:74 M:283 W: Missing Blank Line separator, <400> field identifier  
L:100 M:283 W: Missing Blank Line separator, <400> field identifier  
L:106 M:283 W: Missing Blank Line separator, <400> field identifier  
L:112 M:283 W: Missing Blank Line separator, <400> field identifier  
L:118 M:283 W: Missing Blank Line separator, <400> field identifier  
L:122 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
L:123 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
L:125 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6  
L:128 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:6  
L:128 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:128 M:112 C: (48) String data converted to lower case,  
L:128 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:20 SEQ:6